

# FMRI Data Analysis: Principles & Practice

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SSCC / NIMH / NIH / DHHS / USA / EARTH



<http://afni.nimh.nih.gov/pub/tmp/Kiel2007/>

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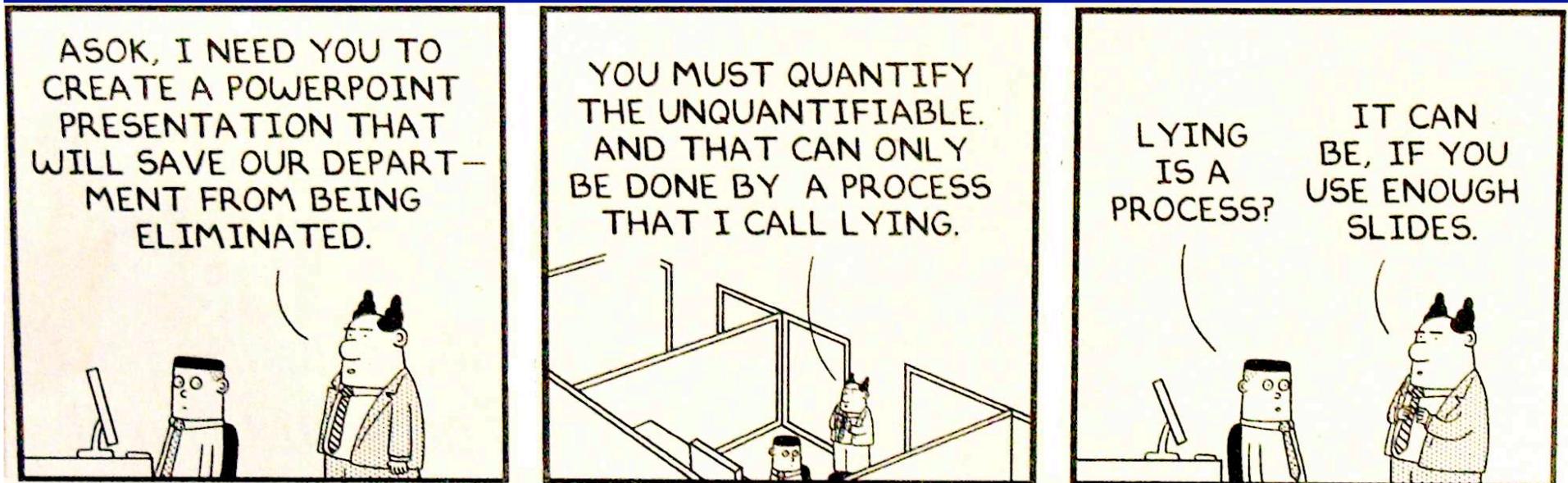
# Ultimate Conclusions First

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- FMRI data analysis is built upon many assumptions, arbitrary parameters, and complex software
  - Don't believe the functional activation maps blindly — check the results by “playing” with the data
- FMRI is an intricate process, from acquisition to analysis to interpretation
  - Doing it well requires a team of experts who work well together

# Warnings & Caveats

- This talk: brief outline of a complex topic
  - I usually spend a week teaching this stuff!



- Almost everything I say herein has an exception, or a complication, or both
  - *and*, opinions differ on some of these issues

# Principles: Modeling

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- Data analysis **always** takes place in the context of a mathematical/statistical model
- Model relates the properties of the system being observed to the numbers that are actually measured
  - Sometimes the model is implicit in the analysis algorithm, rather than being explicitly stated
  - Model must take into account properties of the measurement system
- Models relating fMRI signals to neural activity are complex and **tentative**

# Principles: Data Quality

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- FMRI data are **full of rubbish (Abfall)**:
  - Signal changes with neuronal activation are small (similar to noise magnitude)
  - MRI signal is several levels of indirection away from neuronal changes of interest
- Numerous other signal fluctuations of non-neural origin have similar or greater magnitude:
  - Ghosting, warping, small head movements, **scanner imperfections**, heartbeat, breathing, long-term drifts, signal dropouts, signal spikes, *et cetera*

# Conclusions from Principles

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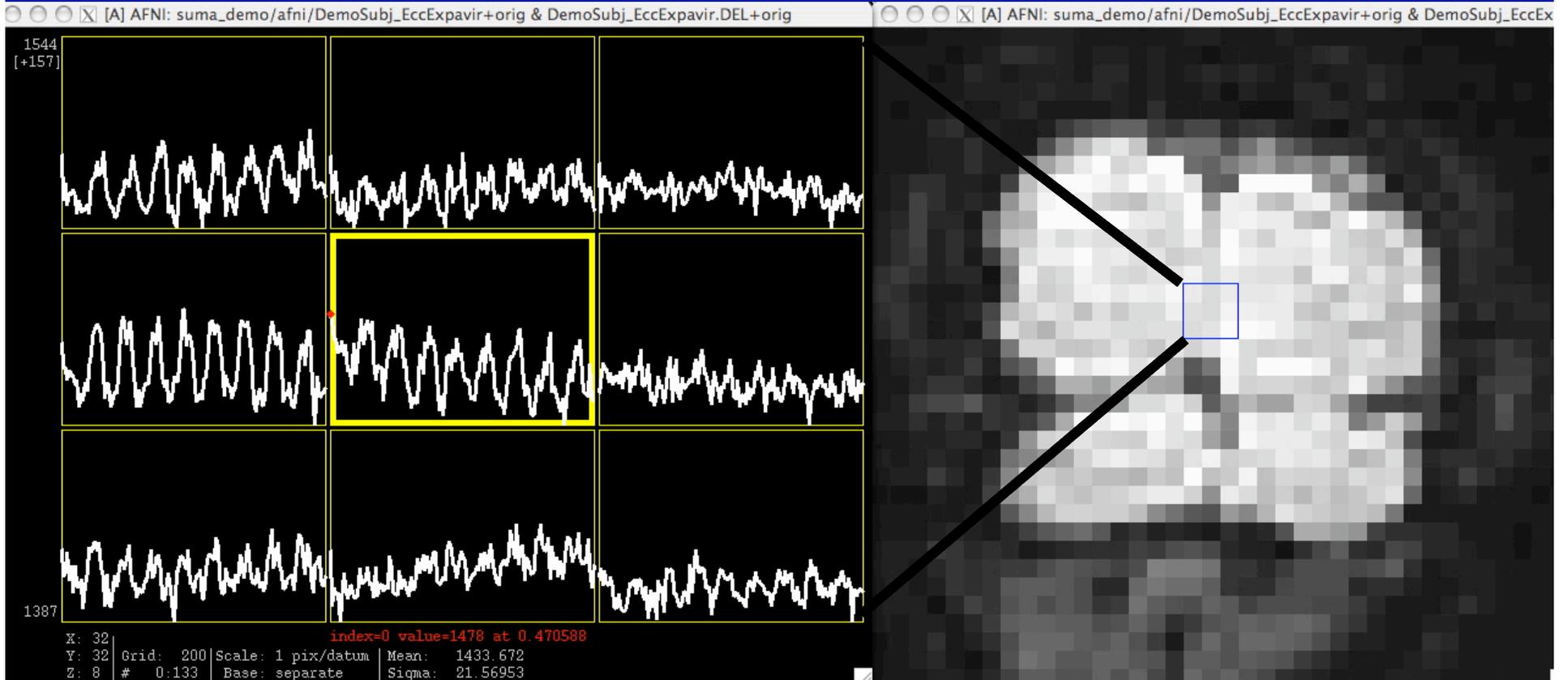
- It is better to state the mathematical model rather than implicitly rely on an algorithm
  - To understand what is being computed
- It is important to try to reduce the rubbish in the data
  - Reduce it at the source *and* in the analysis
  - More data is better (to average out the rubbish)
- It is important to examine the processed data visually at each step in the analysis, to ensure that nothing bad has happened
  - You should understand the process and results

# The Data

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- 10,000..50,000 image voxels inside brain (resolution  $\approx$  2-3 mm)
- 100..1000+ time points in each voxel (time step  $\approx$  2 s)
  - Some of which may be heavily contaminated by subject movement
- Also know timing of stimuli delivered to subject (*etc*)
  - Behavioral, physiological data?
- Hopefully, some hypothesis
  - What are you looking for?

# Sample Data: Visual Area V1



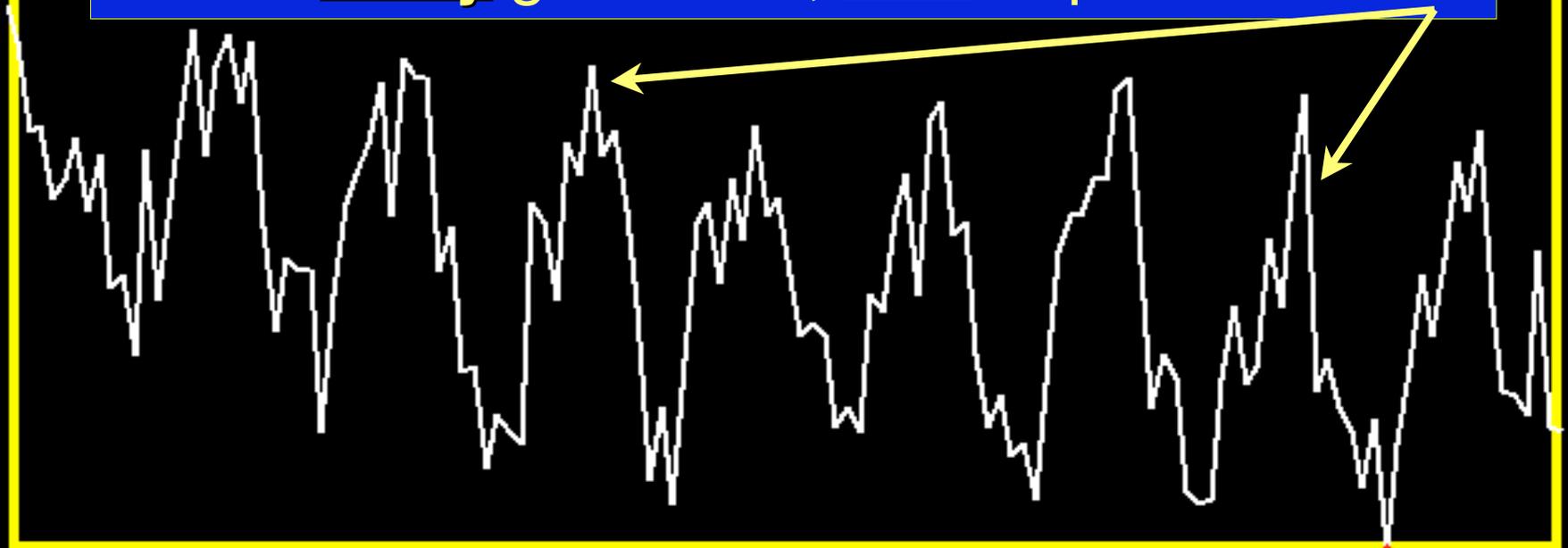
Graphs of 3x3 voxels  
through time

One slice at one time;  
Blue box shows  
graphed voxels

# Same Data as Last Slide

1497.4  
[+110.4]

This is really good data; N.B.: repetitions differ



1387

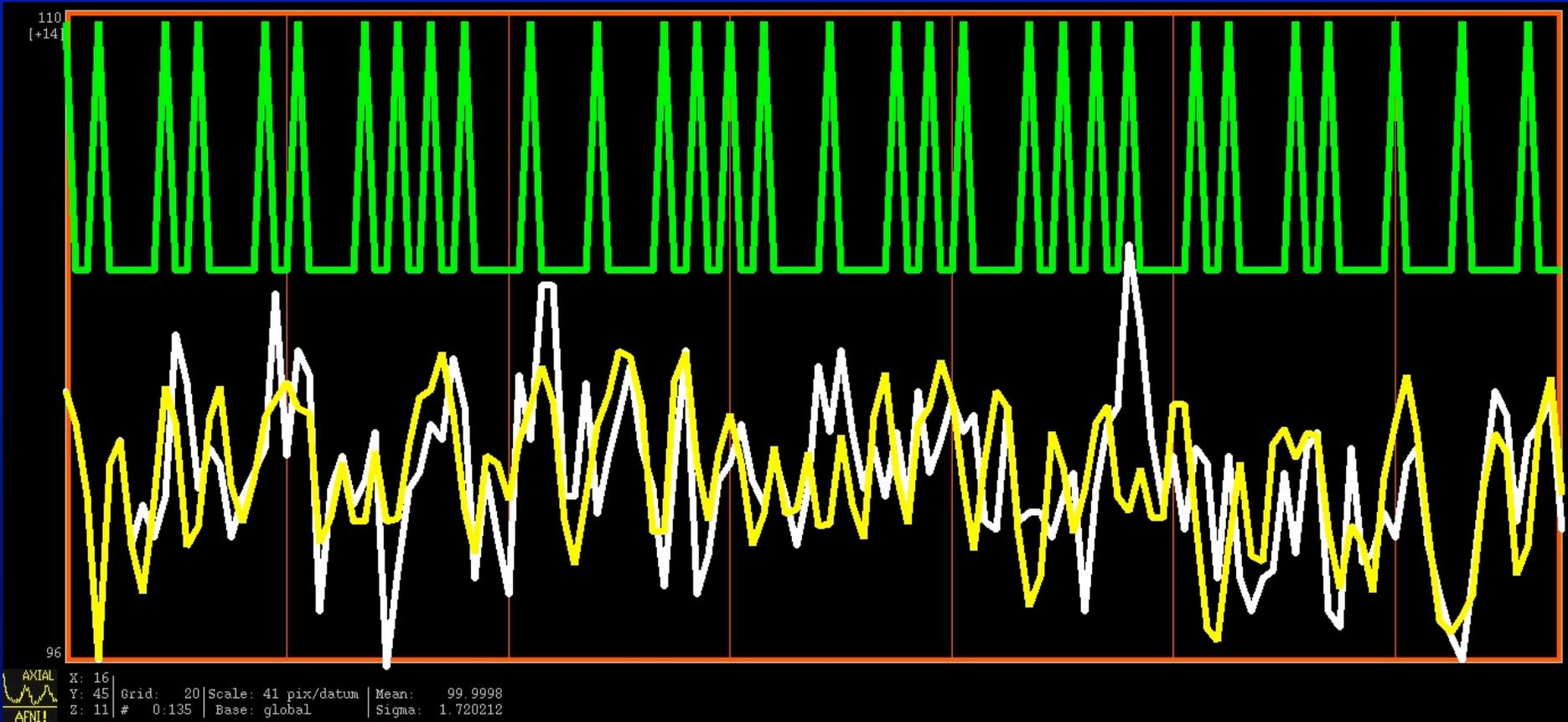
X: 32 | index=118 value=1387 at 236.4706  
Y: 32 | Grid: 200 | Scale: 2.5 pix/datum | Mean: 1433.672  
Z: 8 | # 0:133 | Base: separate | Sigma: 21.56953

Blowup of central time series graph:  
about 7% signal change with a very  
powerful periodic neural stimulus

Block design  
experimental  
paradigm: visual  
stimulation

# Event-Related Data

Four different visual stimuli



- White curve = Data (first 136 TRs)
- Orange curve = Model fit ( $R^2=50\%$ )
- Green = Stimulus timing

Very good fit for ER data ( $R^2=10-20\%$  more usual).  
Noise is as big as BOLD!

# How fMRI Experiments Are Done

- Alternate subject's neural state between 2 (or more) conditions using sensory stimuli, tasks to perform, ...
  - Can only measure relative signals, so must look for *changes* in the signal between the conditions
- Acquire MR images repeatedly during this process
- Search for voxels whose signal time series (*up-&-down*) matches stimulus time series pattern (*on-&-off*)
- Signal changes due to neural activity are small
  - Need about 1000 images in time series (in each slice) ⇒ takes about 1 hour to get fully reliable activation maps
    - Must break image acquisition into shorter "runs" to give the subject and scanner some break time
  - Other small effects can corrupt the results ⇒ postprocess the data to reduce these effects & be careful

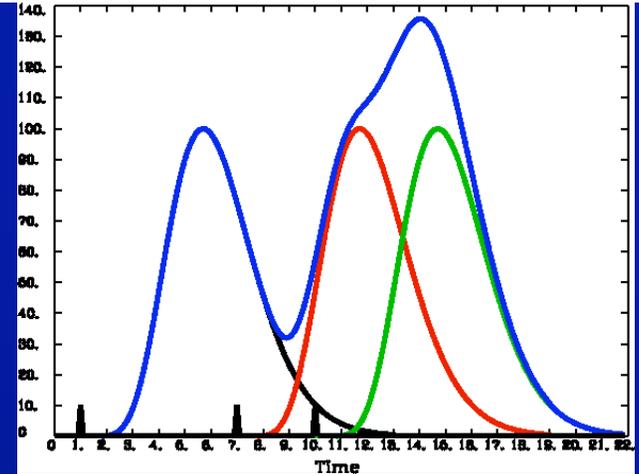
# FMRI Experiment Design and Analysis

*All on one slide!*

- **FMRI experiment design**
  - Single subject or group study? Event-related, block, hybrid event-block?
  - How many types of stimuli? How many of each type? Timing (intra- & inter-stim)?
  - Will experiment show what you are looking for? (**Hint**: bench tests)
  - How many subjects do you need for group analysis? (**Hint**: answer does not have 1 digit)
- **Time series data analysis (individual subjects)**
  - Assembly of images into 4D datasets; Visual & automated checks for bad data
  - Registration of time series images (attempt to correct for subject motion)
  - Smoothing & masking of images; Baseline normalization; Censoring bad data
  - Catenation of imaging runs into one big dataset
  - Fit statistical model of stimulus timing+hemodynamic response to time series data
    - Fixed-shape **or** variable-shape response models
  - Segregation into differentially active blobs
    - Thresholding on statistic + clustering **and/or** Anatomically-defined ROI analysis
  - Visual examination of maps and fitted time series for validity and meaning
- **Group analysis (inter-subject)**
  - Spatial normalization to Talairach-Tournoux atlas (or something like it)
  - Smoothing of fitted parameters
    - Automatic global smoothing + voxel-wise analysis **or** ROI averaging
  - ANOVA to combine and contrast activation magnitudes from the various subjects
  - Visual examination of results (usually followed by confusion)
  - Write paper, argue w/ co-authors, submit paper, argue with referees, publish paper, ...

# Experiment Design - Blocks

- Hemodynamic (fMRI) response
  - peak = 4-6 s after neural activation
  - width = 4-5 s for brief (< 1 s) activation
  - $\Rightarrow$  two separate activations less than 12-15 s apart will have their responses overlap and add up (approximately)
- Block design experiments: Extended activation, or multiple closely-spaced (< 2-3 s apart) activations
  - Multiple fMRI responses accumulate  $\Rightarrow$  big response
  - But: can't distinguish separate but closely-spaced activations
    - Stimulus = “**subject sees a face for 1 s, presses button #1 if male, #2 if female**”; faces every 2 s for a 20 s block, then 20 s of “**rest**”, etc.
    - What to do about trials where the subject makes a mistake?
    - Neurally different than correct trials, but there is no way to separate out the activations when the hemodynamics blurs so much in time.



# Experiment Design - Event-Related

- Separate activations in time so can model fMRI response from each separately, as needed
- Need to make inter-stimulus gaps vary (“jitter”) if there is any time overlap in their fMRI response curves: if events are closer than 12-15 s in time
  - Otherwise, tail of event #x always overlaps head of event #x+1 in same way  $\Rightarrow$  amplitude of response in tail of #x can't be told from response in head of #x+1
- You cannot treat every single event as a distinct entity whose response is to be calculated separately!
  - You must group events into classes, and assume that all events in the same class evoke the same response.
  - Approximate rule: 25+ events per class (with emphasis on the '+')
  - There is just too much noise in fMRI to be able to get an accurate activation map from a single event!

# Experiment Design - Block/Event

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- Long “blocks” are situations where you set up some continuing condition for the subject
- Within a block, multiple distinct events; *Example*:
  - Event stimulus is a picture of a face
  - Block condition is instruction on what the subject is to do when he sees the face:
    - Condition A: press button #1 for male, #2 for female
    - Condition B: press button #1 if face is angry, #2 if face is happy
- Event stimuli in the two conditions may be identical
  - It is the instructional+attentional modulation between the two conditions that is the goal of such a study
  - Perhaps you have two groups of subjects (patients and controls) which respond differently in bench tests
  - You want to find neural substrates for these differences

## 3D Individual Subject Analysis

Assemble images into 4D datasets (e.g., NIfTI-1)

to3d  
OR  
can do at NIH scanners

Check images for quality (visual & automatic)

afni + 3dToutcount + 3dDespike

Register (realign) images

3dvolreg  
OR  
3dWarpDrive

Smooth images spatially

3dmerge (optional)  
OR  
3dBlurToFWHM

Mask out non-brain parts of images

3dAutomask + 3dcalc (optional)

Normalize time series baseline to 100 (for %-izing)

3dTstat + 3dcalc  
(optional: could  
be done post-fit)

Fit stimulus timing+hemodynamic model to time series

- Catenates imaging runs, removes residual movement effects, computes response sizes and inter-stimulus contrasts

3dDeconvolve

Segregate into differentially “activated” blobs

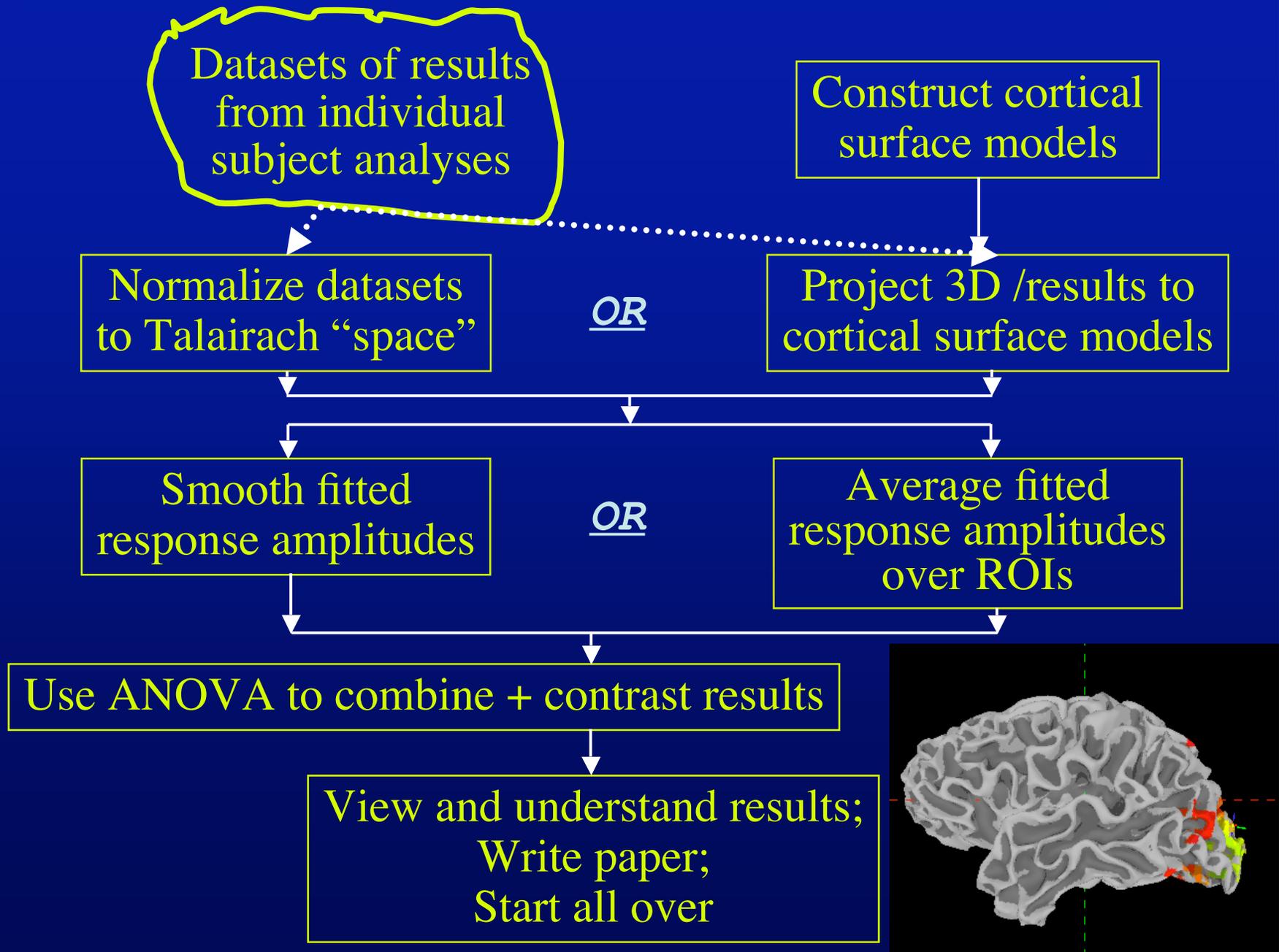
Alphasim + 3dmerge  
OR  
Extraction from ROIs

Look at results, and **think** (e.g., play with thresholds)

afni  
AND  
your personal brain

... to group analysis (next page)

## Group Analysis: in 3D or on folded 2D cortex models



# Fundamental Principles Underlying Most FMRI Analyses (esp. GLM): HRF $\otimes$ Blobs

- Hemodynamic Response Function
  - Convolution model for *temporal* relation between stimulus and response

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- Activation Blobs
  - Contiguous *spatial* regions whose voxel time series fit HRF model
  - e.g., Reject isolated voxels even if HRF model fit is good there

# Temporal Models: Linear Convolution

- **Additivity Assumption:**
  - Input = 2 separated-in-time activations
  - $\Rightarrow$  Output = separated-in-time **sum** of 2 copies of the 1-stimulus response
  - Additivity: approximately true, and improved by caffeine! (Tom Liu, ISMRM 2007)

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- FMRI response to single stimulus is called the **Hemodynamic Response Function (HRF)**
  - Also: **Impulse Response Function (IRF)**

# Hemodynamic Model

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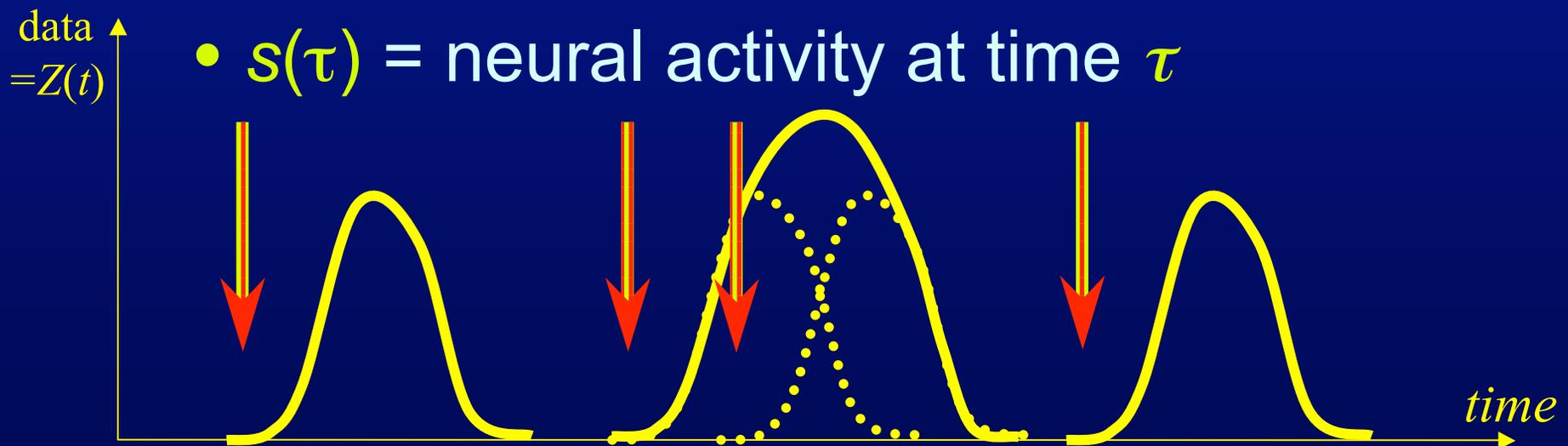
- Measured MRI value in each voxel is **sum** of:
  - Slowly drifting baseline
  - Hemodynamic response that is linearly proportional to “**neural activity**”, delayed and blurred in time
  - Non-neural physiological “noise” due to respiration and blood flow pulsations through the cardiac cycle
  - Residual effects from uncorrectable subject motion and unmeasured scanner hardware fluctuations
  - White noise from random (thermal) currents in the body and the scanner
- Imaging is assumed perfect (no rubbish)
  - Or at least is fixed up in preprocessing steps

# Hemodynamic Model

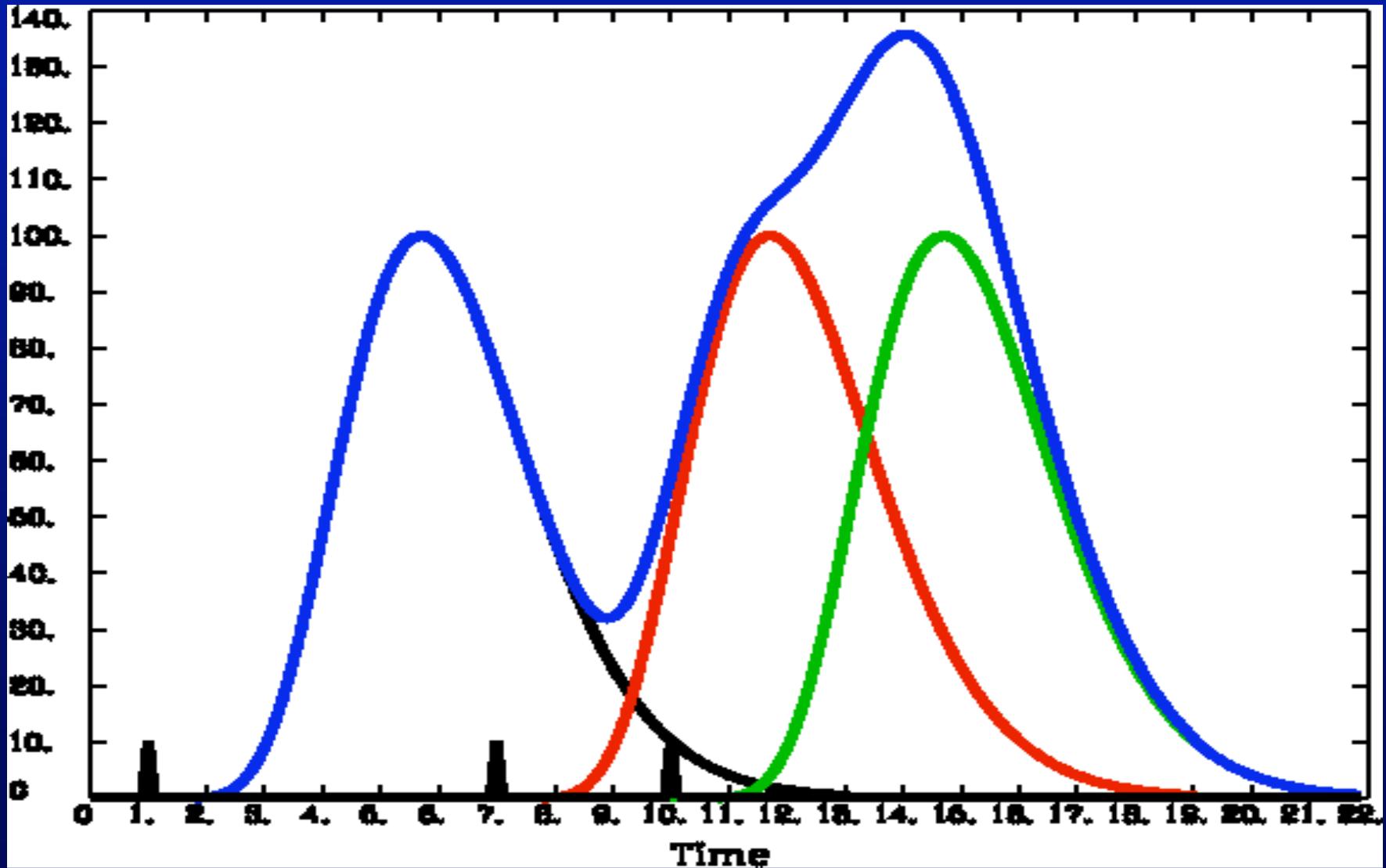
- Linear shift-invariant model for single voxel time series:

$$\text{data} = Z(t) = \text{baseline}(t) + \sum_{\tau=0}^t h(t - \tau)s(\tau) + \text{noise}(t)$$

- $h(t)$  = hemodynamic response at time  $t$  after neural activity
- $s(\tau)$  = neural activity at time  $\tau$



# HRF Model Response to 3 Separate Brief Activations



# Ways to Use This Model

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- Assume  $s(t)$  is known, and then
  - Assume  $h(t)$  is known except for amplitude  $\Rightarrow$  correlation method or fixed shape regression
  - Assume shape of  $h(t)$  is also unknown  $\Rightarrow$  deconvolution (variable shape) method
  - Assume several different classes of  $s(t)$ 's and correspondingly several different  $h(t)$ 's  $\Rightarrow$  generic linear model (GLM)
- Assume  $h(t)$  is known, and find  $s(t)$   
 $\Rightarrow$  inverse FMRI
- Try to find both  $h(t)$  and  $s(t)$   
 $\Rightarrow$  blind deconvolution

# FMRI as Pattern Matching

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- HRF = mathematical model relating what we know (stimulus timing and image data) to what we want to know (location, amount, ..., of neural activity)
- Given data, use this model to solve for unknown parameters in the neural activity (e.g., where, how much, ...)
  - Solving: via multivariate regression
- Then test for statistical significance
- The basis for most published FMRI

# HRF Model Equations

$$h(t) = a \cdot t^b e^{-t/c}$$

Simplest model: fixed shape  
Unknown =  $a$  [ $b$  &  $c$  fixed]

$$h(t) = a_0 \cdot t^b e^{-t/c} + a_1 \cdot \frac{d}{dt} \left[ t^b e^{-t/c} \right]$$

Next simplest model: derivative allows for time shift  
Unknowns =  $a_0$  and  $a_1$  [ $b$  &  $c$  fixed]

$$h(t) = \sum_{q=1}^Q w_q \Phi_q(t)$$

Expansion in a set of fixed basis functions  $\{\Phi_q(t)\}$  (e.g., Splines, sines, ...);  
Unknowns =  $\{w_q\}$

# Multiple Stimulus Classes

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- Need to calculate HRF (amplitude or amplitude+shape) **separately** for each class of stimulus
- Novice fMRI researcher pitfall: try to use too many stimulus classes
- **Event-related fMRI**: need 25+ events per stimulus class
- **Block design fMRI**: need 10+ blocks per stimulus class

# Spatial Models of Activation

- 10,000..50,000 image voxels in brain

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- Don't really expect activation in a single voxel (usually)

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- Curse of multiple comparisons:
  - If have 10,000 statistical tests to perform, and 5% give false positive, would have 500 voxels "activated" by pure noise — way way too much!

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- Can group voxels together somehow to manage this curse

# Spatial Grouping Methods

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- Smooth data in space before analysis
  - Apply threshold based on smoothness
- Average data across anatomically-selected regions of interest ROI (before or after analysis)
  - Labor intensive (*i.e.*, send more postdocs)
- Reject isolated small clusters of above-threshold voxels after analysis

# Spatial Smoothing of Data

- Reduces number of comparisons
- Reduces noise (by averaging)
- Reduces spatial resolution
  - Can make fMRI results look PET-ish
  - In that case, why bother gathering high resolution MR images?
- Smart smoothing: average only over nearby brain or gray matter voxels
  - Uses resolution of fMRI cleverly
  - Or: average over selected ROIs
  - Or: cortical surface based smoothing

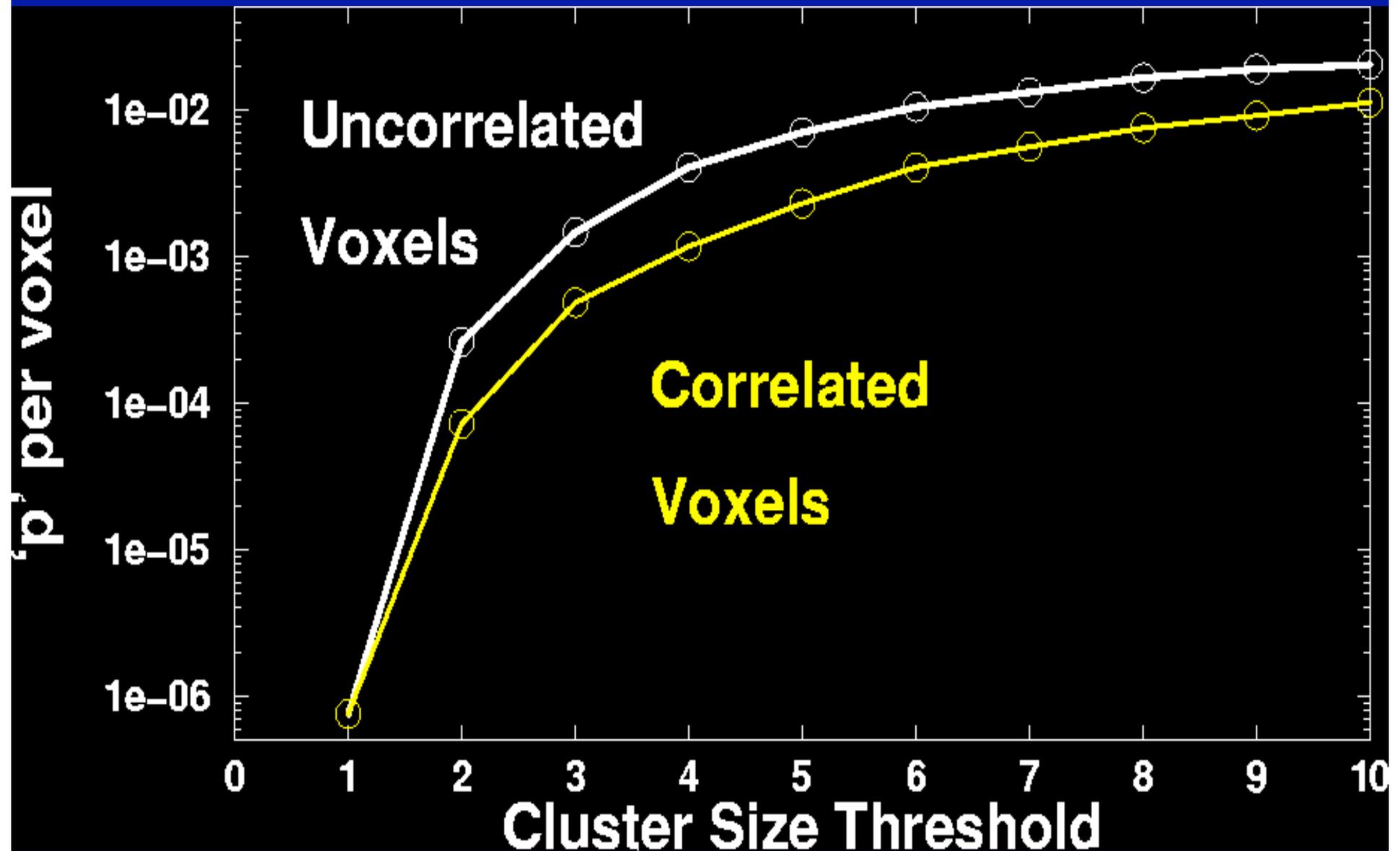
Good things

# Spatial Clustering

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- Analyze data, create statistical map (e.g.,  $t$  statistic in each voxel)
- Threshold map at a lowish  $t$  value, in each voxel separately
- Threshold map by rejecting clusters of voxels below a given size
- Can control false-positive rate by adjusting  $t$  threshold and cluster-size thresholds together

# Cluster-Based Detection



# Allowing for “Noise”

- Physiological “noise”
  - Heartbeat & respiration affect signal
  - Can monitor and try to cancel out

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- Subject head movement
  - After realignment, some effects remain
  - Can include in regression model to reduce effects
  - Task-correlated motion: clever design can help ...

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- Low frequency drifts ( $\leq 0.01$  Hz)
  - Need to include in baseline model

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- Scanner glitches can produce gigantic ( $\geq 10 \sigma$ ) spikes in data
  - Can try to automatically “squash” these

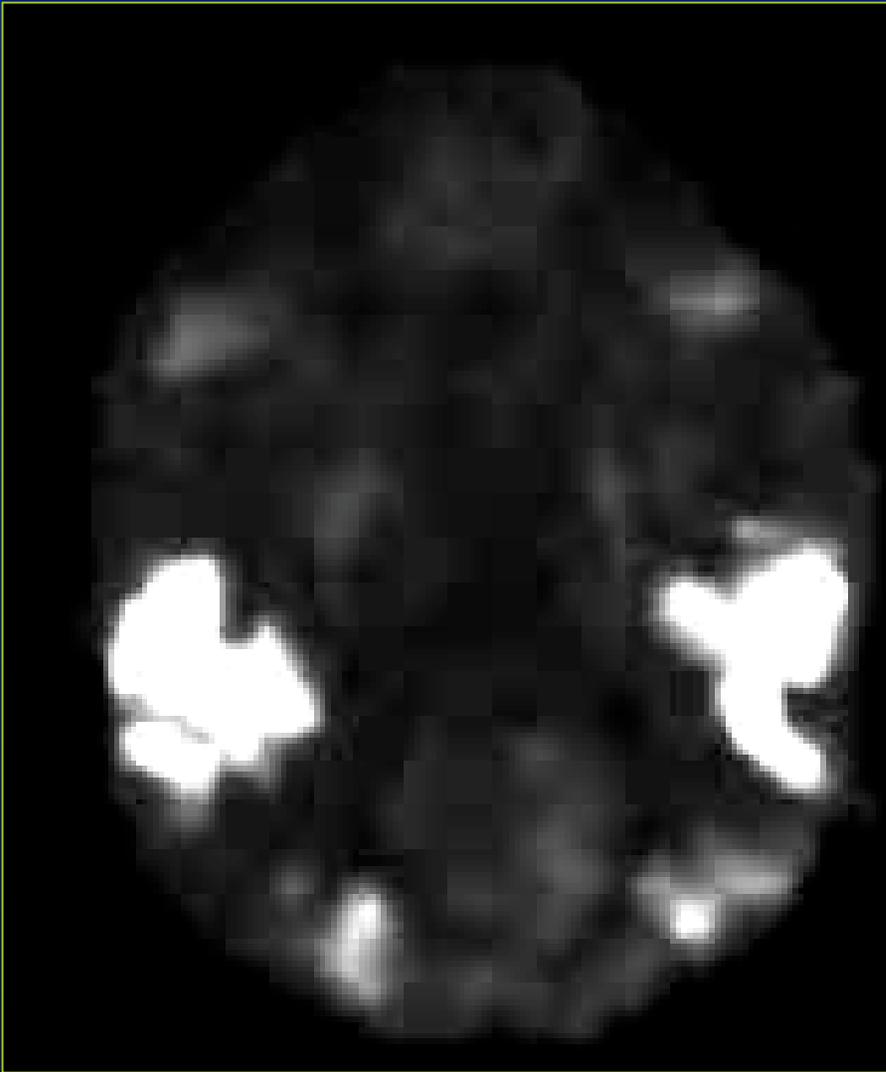
# Rubbish: Things to Look For

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- Errors in setting up the scans
  - Be consistent if scanning same subject on multiple days (e.g., same FOV, slice thickness)
- Large head movements
  - More than a few mm or few degrees
  - Stimulus correlated motion: brain “cap”
- Spikes in the data time series
- Scanner drifts
  - Short term: During long imaging runs
  - Long term: Hardware slowly degrading
    - Set up an fMRI quality check system!
- **Palliative**: real-time image acquisition

# Playing with Your Results

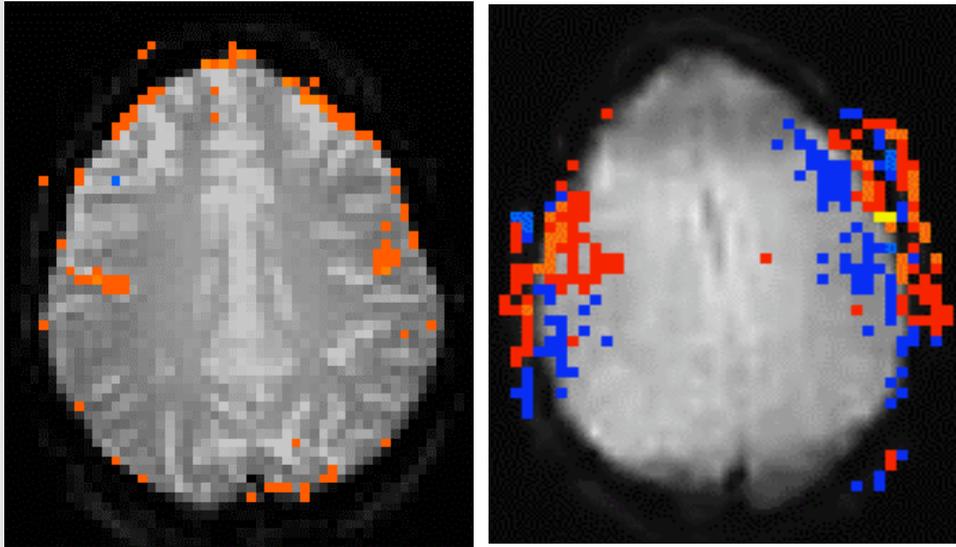
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- Unthresholded **F**-statistic in grayscale
- Animation: loops from very strict threshold to very non-strict
  - No spatial clustering

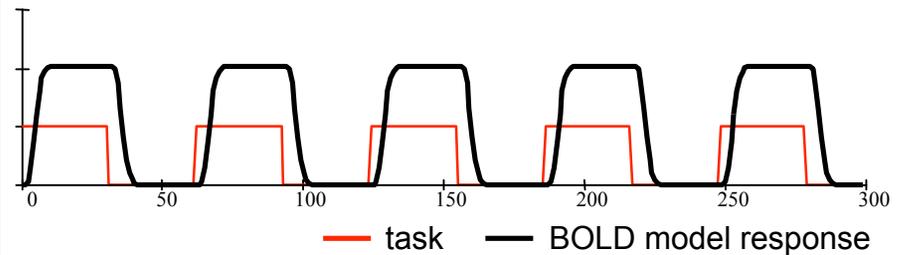
# Correcting for speech-related motion

Overt Speech – 2 block design experiments



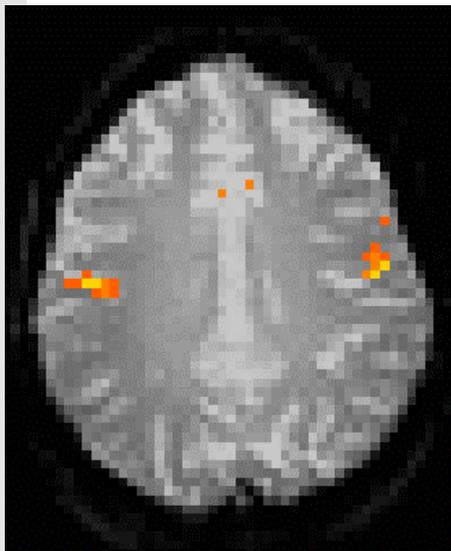
*Overt speech results in large task-related motion artifacts...*

(30s task / 30s rest) (motion highly correlated)

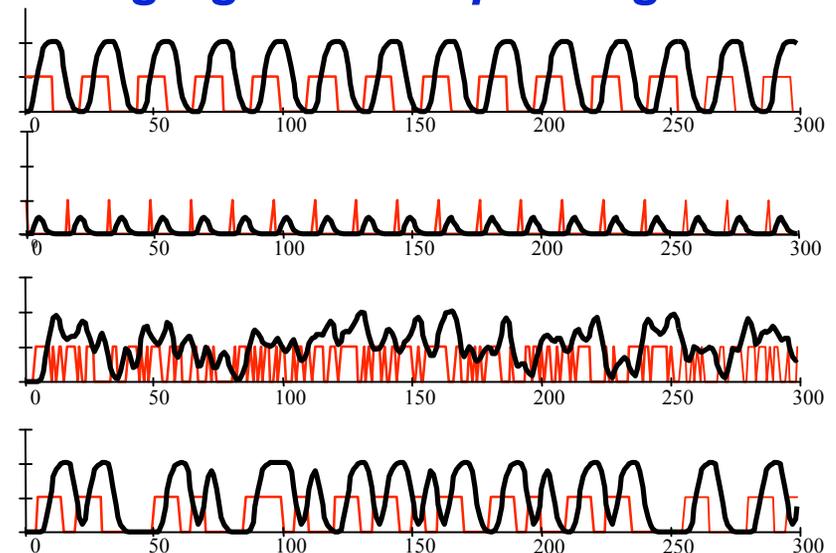


*...These can be reduced by changing the task paradigm*

Overt Speech – event-related design



**Blocked /  
Event-Related  
(low correlation  
with motion)**

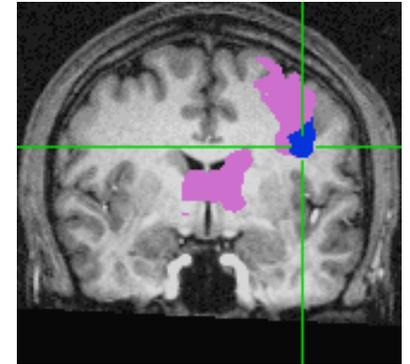
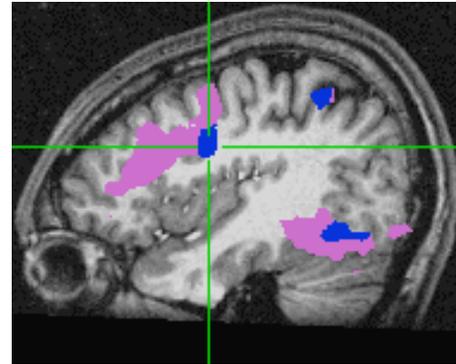
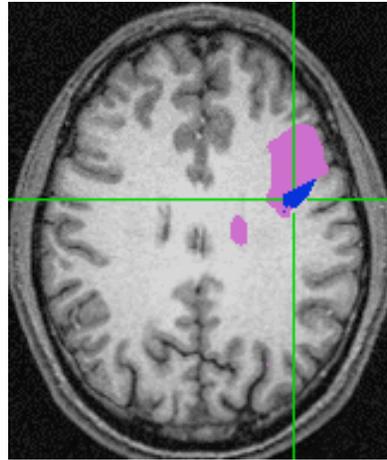


# Differential activation of frontal and temporal cortex by phonemic and category fluency

## *A self-paced overt response fMRI study*

S

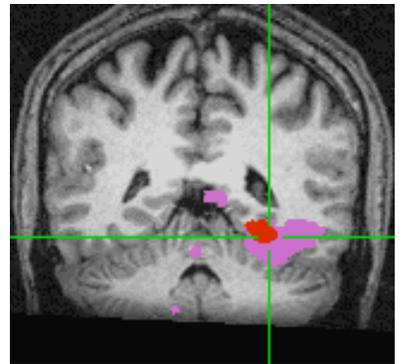
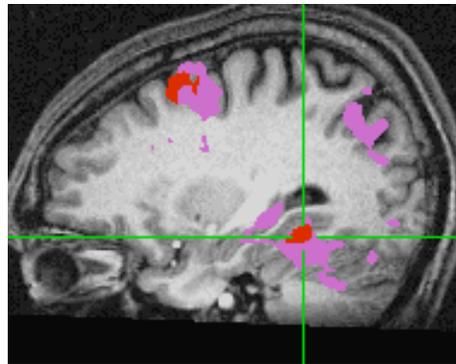
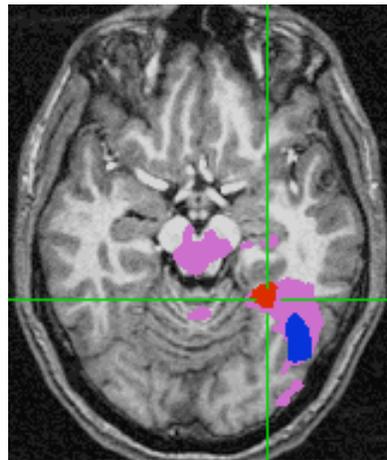
*“Name words that start with the letter S”*



- Blue** = more active for “letters”
- Red** = more active for “categories”
- Pink** = equal activity in both tasks

Animals

*“Name as many animals as you can”*



*Task-related motion artifacts reduced by using 10s ON/10s OFF block design*

# Software Tools

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- What package to use?
  - Sociological answer: the one your neighbors are using (so you can ask them for help)
  - Having a support system in place is crucial!
- **SPM**: most widely used at present
- **AFNI**: flexible, customizable
  - and has the coolest logo .....
- **FSL**: solid package from Oxford
- Numerous other good packages out there
  - Mix-and-match with NIfTI-1 common data format
- Commercial products: MedX, Brain Voyager



# Second Set of Conclusions

- FMRI data contain features that are about the same size as the BOLD signal *and* are poorly understood
- Thus: There are many “reasonable” ways to analyze FMRI data
  - Depending on the assumptions about the brain, the signal, and the noise
- Conclusions: **Understand what you are doing & Look at your data**
  - Or you will do something stupid

# Finally ... Thanks

- The list of people I should thank is not quite endless ...

MM Klosek. JS Hyde. JR Binder. EA DeYoe. SM Rao.  
EA Stein. A Jesmanowicz. MS Beauchamp. BD Ward.

KM Donahue. PA Bandettini. AS Bloom. T Ross.

M Huerta. ZS Saad. K Ropella. B Knutson. J Bobholz.

G Chen. RM Birn. J Ratke. PSF Bellgowan. J Frost.

K Bove-Bettis. R Doucette. RC Reynolds. PP Christidis.

LR Frank. R Desimone. L Ungerleider. KR Hammett.

DS Cohen. DA Jacobson. EC Wong. D Glen.

*And YOU, the audience ...*

<http://afni.nimh.nih.gov/pub/tmp/Kiel2007/>